

SEQUENCE LISTING

<110> MILLENIUM PHARMACEUTICALS, INC.

<120> SPLEEN TYROSINE KINASE CATALYTIC DOMAIN: CRYSTAL
STRUCTURE AND BINDING POCKETS THEREOF

<130> MNM/001 PCT

<140> PCT/US03/32812

<141> 2003-10-16

<150> 60/419,382

<151> 2002-10-16

<160> 11

<170> PatentIn Ver. 3.2

<210> 1

<211> 635

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Ser Ser Gly Met Ala Asp Ser Ala Asn His Leu Pro Phe Phe
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Phe Gly Asn Ile Thr Arg Glu Glu Ala Glu Asp Tyr Leu Val Gln Gly
20 25 30

Gly Met Ser Asp Gly Leu Tyr Leu Leu Arg Gln Ser Arg Asn Tyr Leu
35 40 45

Gly Gly Phe Ala Leu Ser Val Ala His Gly Arg Lys Ala His His Tyr
50 55 60

Thr Ile Glu Arg Glu Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Arg
65 70 75 80

Thr His Ala Ser Pro Ala Asp Leu Cys His Tyr His Ser Gln Glu Ser
85 90 95

Asp Gly Leu Val Cys Leu Leu Lys Lys Pro Phe Asn Arg Pro Gln Gly
100 105 110

Val Gln Pro Lys Thr Gly Pro Phe Glu Asp Leu Lys Glu Asn Leu Ile
115 120 125

Arg Glu Tyr Val Lys Gln Thr Trp Asn Leu Gln Gly Gln Ala Leu Glu
130 135 140

Gln Ala Ile Ile Ser Gln Lys Pro Gln Leu Glu Lys Leu Ile Ala Thr
145 150 155 160

Thr Ala His Glu Lys Met Pro Trp Phe His Gly Lys Ile Ser Arg Glu
165 170 175

Glu Ser Glu Gln Ile Val Leu Ile Gly Ser Lys Thr Asn Gly Lys Phe
180 185 190

Leu Ile Arg Ala Arg Asp Asn Asn Gly Ser Tyr Ala Leu Cys Leu Leu

195					200					205					
His	Glu	Gly	Lys	Val	Leu	His	Tyr	Arg	Ile	Asp	Lys	Asp	Lys	Thr	Gly
210						215					220				
Lys	Leu	Ser	Ile	Pro	Glu	Gly	Lys	Lys	Phe	Asp	Thr	Leu	Trp	Gln	Leu
225					230					235					240
Val	Glu	His	Tyr	Ser	Tyr	Lys	Ala	Asp	Gly	Leu	Leu	Arg	Val	Leu	Thr
				245					250					255	
Val	Pro	Cys	Gln	Lys	Ile	Gly	Thr	Gln	Gly	Asn	Val	Asn	Phe	Gly	Gly
			260					265					270		
Arg	Pro	Gln	Leu	Pro	Gly	Ser	His	Pro	Ala	Thr	Trp	Ser	Ala	Gly	Gly
			275				280					285			
Ile	Ile	Ser	Arg	Ile	Lys	Ser	Tyr	Ser	Phe	Pro	Lys	Pro	Gly	His	Arg
	290					295					300				
Lys	Ser	Ser	Pro	Ala	Gln	Gly	Asn	Arg	Gln	Glu	Ser	Thr	Val	Ser	Phe
305					310					315					320
Asn	Pro	Tyr	Glu	Pro	Glu	Leu	Ala	Pro	Trp	Ala	Ala	Asp	Lys	Gly	Pro
				325					330					335	
Gln	Arg	Glu	Ala	Leu	Pro	Met	Asp	Thr	Glu	Val	Tyr	Glu	Ser	Pro	Tyr
			340					345					350		
Ala	Asp	Pro	Glu	Glu	Ile	Arg	Pro	Lys	Glu	Val	Tyr	Leu	Asp	Arg	Lys
		355					360					365			
Leu	Leu	Thr	Leu	Glu	Asp	Lys	Glu	Leu	Gly	Ser	Gly	Asn	Phe	Gly	Thr
	370					375					380				
Val	Lys	Lys	Gly	Tyr	Tyr	Gln	Met	Lys	Lys	Val	Val	Lys	Thr	Val	Ala
385					390					395					400
Val	Lys	Ile	Leu	Lys	Asn	Glu	Ala	Asn	Asp	Pro	Ala	Leu	Lys	Asp	Glu
				405					410					415	
Leu	Leu	Ala	Glu	Ala	Asn	Val	Met	Gln	Gln	Leu	Asp	Asn	Pro	Tyr	Ile
			420					425					430		
Val	Arg	Met	Ile	Gly	Ile	Cys	Glu	Ala	Glu	Ser	Trp	Met	Leu	Val	Met
		435					440					445			
Glu	Met	Ala	Glu	Leu	Gly	Pro	Leu	Asn	Lys	Tyr	Leu	Gln	Gln	Asn	Arg
	450					455					460				
His	Val	Lys	Asp	Lys	Asn	Ile	Ile	Glu	Leu	Val	His	Gln	Val	Ser	Met
465					470					475					480
Gly	Met	Lys	Tyr	Leu	Glu	Glu	Ser	Asn	Phe	Val	His	Arg	Asp	Leu	Ala
				485					490					495	
Ala	Arg	Asn	Val	Leu	Leu	Val	Thr	Gln	His	Tyr	Ala	Lys	Ile	Ser	Asp
			500					505					510		
Phe	Gly	Leu	Ser	Lys	Ala	Leu	Arg	Ala	Asp	Glu	Asn	Tyr	Tyr	Lys	Ala
		515					520					525			
Gln	Thr	His	Gly	Lys	Trp	Pro	Val	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile

530	535	540
Asn Tyr Tyr Lys Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly Val		
545	550	555 560
Leu Met Trp Glu Ala Phe Ser Tyr Gly Gln Lys Pro Tyr Arg Gly Met		
	565	570 575
Lys Gly Ser Glu Val Thr Ala Met Leu Glu Lys Gly Glu Arg Met Gly		
	580	585 590
Cys Pro Ala Gly Cys Pro Arg Glu Met Tyr Asp Leu Met Asn Leu Cys		
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Trp Thr Tyr Asp Val Glu Asn Arg Pro Gly Phe Ala Ala Val Glu Leu		
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Arg Leu Arg Asn Tyr Tyr Tyr Asp Val Val Asn		
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 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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 <222> (1)
 <223> NAc-Glu

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 <223> c-term amidation

<400> 2
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<210> 3
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
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 1 5

<210> 6
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<210> 8
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<220>
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 1 5

<210> 9
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<223> Description of Artificial Sequence: Synthetic peptide

<400> 9

Asp Tyr Glu Glu Val
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<212> PRT

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<223> Description of Artificial Sequence: Synthetic peptide

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<221> MOD_RES

<222> (5)

<223> Nle

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Tyr Ser Ile Ile Xaa
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<210> 11

<211> 26

<212> PRT

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<220>

<223> Description of Artificial Sequence: Consensus
sequence

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<221> MOD_RES

<222> (6)..(12)

<223> Variable amino acid

<220>

<221> MOD_RES

<222> (14)

<223> Variable amino acid

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<222> (16)

<223> Variable amino acid

<220>

<221> MOD_RES

<222> (20)

<223> Variable amino acid

<400> 11

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1 5 10 15

Cys Gly Thr Xaa Asp Tyr Leu Pro Pro Glu
20 25